

SEQUENCE LISTING

<110> Bristol-Myers Squibb Company

<120> NUCLEIC ACID MOLECULES AND POLYPEPTIDES FOR A HUMAN CATION CHANNEL POLYPEPTIDE

<130> D0187NP

<150> US 60/257,865

<151> 2000-12-21

<160> 24

<170> PatentIn version 3.0

<210> 1

<211> 2186

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (20)..(2011)

<220>

<221> misc_feature

<222> (2150)..(2150)

<223> wherein "n" equals A, C, G, or T.

<400> 1

ctctagatgt acatggagg atg acc gaa aaa acc aat ggt gtg aag agc tcc	52
Met Thr Glu Lys Thr Asn Gly Val Lys Ser Ser	
1 5 10	
cca gcc aat aat cac aac cat cat gca cct cct gcc atc aag gcc aat	100
Pro Ala Asn Asn His Asn His His Ala Pro Pro Ala Ile Lys Ala Asn	
15 20 25	
ggc aaa gat gac cac agg aca agc agc agg cca cac tct gca gct gac	148
Gly Lys Asp Asp His Arg Thr Ser Ser Arg Pro His Ser Ala Ala Asp	
30 35 40	
gat gac acc tcc tca gaa ctg cag agg ctg gca gac gtg gat gcc cca	196
Asp Asp Thr Ser Ser Glu Leu Gln Arg Leu Ala Asp Val Asp Ala Pro	
45 50 55	
cag cag gga agg agt ggc ttc cgc agg ata gtt cgc ctg gtg ggg atc	244
Gln Gln Gly Arg Ser Gly Phe Arg Arg Ile Val Arg Leu Val Gly Ile	
60 65 70 75	
atc aga gaa tgg gcc aac aag aat ttc cga gag gag gaa cct agg cct	292
Ile Arg Glu Trp Ala Asn Lys Asn Phe Arg Glu Glu Glu Pro Arg Pro	
80 85 90	
gac tca ttc ctg gag cgt ttt cgt ggg cct gaa ctg cag act gtg acc	340
Asp Ser Phe Leu Glu Arg Phe Arg Gly Pro Glu Leu Gln Thr Val Thr	
95 100 105	
aca cag gag ggg gat ggc aaa ggc gac aag gat ggc gag gac aaa ggc	388

Thr	Gln	Glu	Gly	Asp	Gly	Lys	Gly	Asp	Lys	Asp	Gly	Glu	Asp	Lys	Gly		
		110					115					120					
acc	aag	aag	aaa	ttt	gaa	cta	ttt	gtc	ttg	gac	cca	gct	ggg	gat	ttg		436
Thr	Lys	Lys	Lys	Phe	Glu	Leu	Phe	Val	Leu	Asp	Pro	Ala	Gly	Asp	Leu		
		125				130					135						
tac	tac	tgc	tgg	cta	ttt	gtc	att	gcc	atg	ccc	gtc	ctt	tac	aac	tgg		484
Tyr	Tyr	Cys	Trp	Leu	Phe	Val	Ile	Ala	Met	Pro	Val	Leu	Tyr	Asn	Trp		
		140			145					150					155		
tgc	ctg	ctg	gtg	gcc	aga	gcc	tgc	ttc	agt	gac	cta	cag	aaa	ggc	tac		532
Cys	Leu	Leu	Val	Ala	Arg	Ala	Cys	Phe	Ser	Asp	Leu	Gln	Lys	Gly	Tyr		
				160					165					170			
tac	ctg	gtg	tgg	ctg	gtg	ctg	gat	tat	gtc	tca	gat	gtg	gtc	tac	att		580
Tyr	Leu	Val	Trp	Leu	Val	Leu	Asp	Tyr	Val	Ser	Asp	Val	Val	Tyr	Ile		
			175					180						185			
gcg	gac	ctc	ttc	atc	cga	ttg	cgc	aca	ggt	ttc	ctg	gag	cag	ggg	ctg		628
Ala	Asp	Leu	Phe	Ile	Arg	Leu	Arg	Thr	Gly	Phe	Leu	Glu	Gln	Gly	Leu		
		190					195					200					
ctg	gtc	aaa	gat	acc	aag	aaa	ctg	cga	gac	aac	tac	atc	cac	acc	ctg		676
Leu	Val	Lys	Asp	Thr	Lys	Lys	Leu	Arg	Asp	Asn	Tyr	Ile	His	Thr	Leu		
		205				210					215						
cag	ttc	aag	ctg	gat	gtg	gct	tcc	atc	atc	ccc	act	gac	ctg	atc	tat		724
Gln	Phe	Lys	Leu	Asp	Val	Ala	Ser	Ile	Ile	Pro	Thr	Asp	Leu	Ile	Tyr		
		220			225					230					235		
ttt	gct	gtg	gac	atc	cac	agc	cct	gag	gtg	cgc	ttc	aac	cgc	ctg	ctg		772
Phe	Ala	Val	Asp	Ile	His	Ser	Pro	Glu	Val	Arg	Phe	Asn	Arg	Leu	Leu		
			240					245						250			
cac	ttt	gcc	cgc	atg	ttt	gag	ttc	ttt	gac	cgg	aca	gag	aca	cgc	acc		820
His	Phe	Ala	Arg	Met	Phe	Glu	Phe	Phe	Asp	Arg	Thr	Glu	Thr	Arg	Thr		
		255						260						265			
aac	tac	cct	aac	atc	ttc	cgc	atc	agc	aac	ctt	gtc	ctc	tac	atc	ttg		868
Asn	Tyr	Pro	Asn	Ile	Phe	Arg	Ile	Ser	Asn	Leu	Val	Leu	Tyr	Ile	Leu		
		270					275						280				
gtc	atc	atc	cac	tgg	aat	gcc	tgc	atc	tat	tat	gcc	atc	tcc	aaa	tcc		916
Val	Ile	Ile	His	Trp	Asn	Ala	Cys	Ile	Tyr	Tyr	Ala	Ile	Ser	Lys	Ser		
		285				290					295						
ata	ggc	ttt	ggg	gtc	gac	acc	tgg	gtt	tac	cca	aac	atc	act	gac	cct		964
Ile	Gly	Phe	Gly	Val	Asp	Thr	Trp	Val	Tyr	Pro	Asn	Ile	Thr	Asp	Pro		
		300			305					310					315		
gag	tat	ggc	tac	ctg	gct	agg	gaa	tac	atc	tat	tgc	ctt	tac	tgg	tcc		1012
Glu	Tyr	Gly	Tyr	Leu	Ala	Arg	Glu	Tyr	Ile	Tyr	Cys	Leu	Tyr	Trp	Ser		
				320				325						330			
aca	ctg	act	ctc	act	acc	att	ggg	gag	aca	cca	ccc	cct	gta	aag	gat		1060
Thr	Leu	Thr	Thr	Thr	Ile	Gly	Glu	Thr	Pro	Pro	Pro	Pro	Val	Lys	Asp		
			335				340						345				
gag	gag	tac	cta	ttt	gtc	atc	ttt	gac	ttc	ctg	att	ggc	gtc	ctc	atc		1108
Glu	Glu	Tyr	Leu	Phe	Val	Ile	Phe	Asp	Phe	Leu	Ile	Gly	Val	Leu	Ile		

1156
 1204
 1252
 1300
 1348
 1396
 1444
 1492
 1540
 1588
 1636
 1684
 1732
 1780
 1828

350	355	360	
ttt gcc acc atc gtg gga aat gtg ggc tcc atg atc tcc aac atg aat Phe Ala Thr Ile Val Gly Asn Val Gly Ser Met Ile Ser Asn Met Asn 365 370 375			1156
gcc acc cgg gca gag ttc cag gct aag atc gat gcc gtg aaa cac tac Ala Thr Arg Ala Glu Phe Gln Ala Lys Ile Asp Ala Val Lys His Val 380 385 390 395			1204
atg cag ttc cga aag gtc agc aag ggg atg gaa gcc aag gtc att agg Met Gln Phe Arg Lys Val Ser Lys Gly Met Glu Ala Lys Val Ile Arg 400 405 410			1252
tgg ttt gac tac ttg tgg acc aat aag aag aca gtg gat gag cga gaa Trp Phe Asp Tyr Leu Trp Thr Asn Lys Lys Thr Val Asp Glu Arg Glu 415 420 425			1300
att ctc aag aat ctg cca gcc aag ctc agg gct gag ata gcc acc aat Ile Leu Lys Asn Leu Pro Ala Lys Leu Arg Ala Glu Ile Ala Thr Asn 430 435 440			1348
gtc cac ttg tcc aca ctc aag aaa gtg cgc atc ttc cat gat tgt gag Val His Leu Ser Thr Leu Lys Lys Val Arg Ile Phe His Asp Cys Glu 445 450 455			1396
gct ggc ctg ctg gta gag ctg gta ctg aaa ctc cgt cct cag gtc ttc Ala Gly Leu Leu Val Glu Leu Val Leu Lys Leu Arg Pro Gln Val Phe 460 465 470 475			1444
agt cct ggg gat tac att tgc cgc aaa ggg gac atc gcc aag gag atg Ser Pro Gly Asp Tyr Ile Cys Arg Lys Gly Asp Ile Gly Lys Glu Met 480 485 490			1492
tac atc att aag gag ggc aaa ctg gca gtg gtg gct gat gat ggt gtg Tyr Ile Ile Lys Glu Gly Lys Leu Ala Val Val Ala Asp Asp Gly Val 495 500 505			1540
act cag tat gct ctg ctg tcg gct gga agc tgc ttt ggc gag atc agt Thr Gln Tyr Ala Leu Leu Ser Ala Gly Ser Cys Phe Gly Glu Ile Ser 510 515 520			1588
atc ctt aac att aag ggc agt aaa atg ggc aat cga cgc aca gct aat Ile Leu Asn Ile Lys Gly Ser Lys Met Gly Asn Arg Arg Thr Ala Asn 525 530 535			1636
atc cgc agc ctg ggc tac tca gat ctc ttc tgc ttg tcc aag gat gat Ile Arg Ser Leu Gly Tyr Ser Asp Leu Phe Cys Leu Ser Lys Asp Asp 540 545 550 555			1684
ctt atg gaa gct gtg act gag tac cct gat gcc aag aaa gtc cta gaa Leu Met Glu Ala Val Thr Glu Tyr Pro Asp Ala Lys Lys Val Leu Glu 560 565 570			1732
gag agg ggt cgg gag atc ctc atg aag gag gga ctg ctg gat gag aac Glu Arg Gly Arg Glu Ile Leu Met Lys Glu Gly Leu Leu Asp Glu Asn 575 580 585			1780
gaa gtg gca acc agc atg gag gtc gac gtg cag gag aag cta ggg cag Glu Val Ala Thr Ser Met Glu Val Asp Val Gln Glu Lys Leu Gly Gln 590 595 600			1828

ctg gag acc aac atg gaa acc ttg tac act cgc ttt ggc cgc ctg ctg 1876
 Leu Glu Thr Asn Met Glu Thr Leu Tyr Thr Arg Phe Gly Arg Leu Leu
 605 610 615

gct gag tac acg ggg gcc cag cag aag ctc aag cag cgc atc aca gtt 1924
 Ala Glu Tyr Thr Gly Ala Gln Gln Lys Leu Lys Gln Arg Ile Thr Val
 620 625 630 635

ctg gaa acc aag atg aaa cag aac aat gaa gat gac tac ctg tct gat 1972
 Leu Glu Thr Lys Met Lys Gln Asn Asn Glu Asp Asp Tyr Leu Ser Asp
 640 645 650

ggg atg aac agc cct gag ctg gct gct gct gac gag cca taagacctgg 2021
 Gly Met Asn Ser Pro Glu Leu Ala Ala Ala Asp Glu Pro
 655 660

ggcccaactg cctctccagc attggccttg gccttgatcc cagaagctag aggagctatt 2081

tagatctccg gatttacatg cattaccctc atgttccctg aattctccca aaagtctctc 2141

tgaccctgng tttttggcct aaacatccaa gattccgcct cggat 2186

<210> 2

<211> 664

<212> PRT

<213> Homo sapiens

<220>

<221> misc feature

<222> (2150)..(2150)

<223> wherein "n" equals A, C, G, or T.

<400> 2

Met Thr Glu Lys Thr Asn Gly Val Lys Ser Ser Pro Ala Asn Asn His
 1 5 10 15

Asn His His Ala Pro Pro Ala Ile Lys Ala Asn Gly Lys Asp Asp His
 20 25 30

Arg Thr Ser Ser Arg Pro His Ser Ala Ala Asp Asp Asp Thr Ser Ser
 35 40 45

Glu Leu Gln Arg Leu Ala Asp Val Asp Ala Pro Gln Gln Gly Arg Ser
 50 55 60

Gly Phe Arg Arg Ile Val Arg Leu Val Gly Ile Ile Arg Glu Trp Ala
 65 70 75 80

Asn Lys Asn Phe Arg Glu Glu Glu Pro Arg Pro Asp Ser Phe Leu Glu
 85 90 95

Arg Phe Arg Gly Pro Glu Leu Gln Thr Val Thr Thr Gln Glu Gly Asp

100

105

110

Gly Lys Gly Asp Lys Asp Gly Glu Asp Lys Gly Thr Lys Lys Lys Phe
 115 120 125

Glu Leu Phe Val Leu Asp Pro Ala Gly Asp Leu Tyr Tyr Cys Trp Leu
 130 135 140

Phe Val Ile Ala Met Pro Val Leu Tyr Asn Trp Cys Leu Leu Val Ala
 145 150 155 160

Arg Ala Cys Phe Ser Asp Leu Gln Lys Gly Tyr Tyr Leu Val Trp Leu
 165 170 175

Val Leu Asp Tyr Val Ser Asp Val Val Tyr Ile Ala Asp Leu Phe Ile
 180 185 190

Arg Leu Arg Thr Gly Phe Leu Glu Gln Gly Leu Leu Val Lys Asp Thr
 195 200 205

Lys Lys Leu Arg Asp Asn Tyr Ile His Thr Leu Gln Phe Lys Leu Asp
 210 215 220

Val Ala Ser Ile Ile Pro Thr Asp Leu Ile Tyr Phe Ala Val Asp Ile
 225 230 235 240

His Ser Pro Glu Val Arg Phe Asn Arg Leu Leu His Phe Ala Arg Met
 245 250 255

Phe Glu Phe Phe Asp Arg Thr Glu Thr Arg Thr Asn Tyr Pro Asn Ile
 260 265 270

Phe Arg Ile Ser Asn Leu Val Leu Tyr Ile Leu Val Ile Ile His Trp
 275 280 285

Asn Ala Cys Ile Tyr Tyr Ala Ile Ser Lys Ser Ile Gly Phe Gly Val
 290 295 300

Asp Thr Trp Val Tyr Pro Asn Ile Thr Asp Pro Glu Tyr Gly Tyr Leu
 305 310 315 320

Ala Arg Glu Tyr Ile Tyr Cys Leu Tyr Trp Ser Thr Leu Thr Leu Thr
 325 330 335

Thr Ile Gly Glu Thr Pro Pro Pro Val Lys Asp Glu Glu Tyr Leu Phe
 340 345 350

Val Ile Phe Asp Phe Leu Ile Gly Val Leu Ile Phe Ala Thr Ile Val
355 360 365

Gly Asn Val Gly Ser Met Ile Ser Asn Met Asn Ala Thr Arg Ala Glu
370 375 380

Phe Gln Ala Lys Ile Asp Ala Val Lys His Tyr Met Gln Phe Arg Lys
385 390 395 400

Val Ser Lys Gly Met Glu Ala Lys Val Ile Arg Trp Phe Asp Tyr Leu
405 410 415

Trp Thr Asn Lys Lys Thr Val Asp Glu Arg Glu Ile Leu Lys Asn Leu
420 425 430

Pro Ala Lys Leu Arg Ala Glu Ile Ala Thr Asn Val His Leu Ser Thr
435 440 445

Leu Lys Lys Val Arg Ile Phe His Asp Cys Glu Ala Gly Leu Leu Val
450 455 460

Glu Leu Val Leu Lys Leu Arg Pro Gln Val Phe Ser Pro Gly Asp Tyr
465 470 475 480

Ile Cys Arg Lys Gly Asp Ile Gly Lys Glu Met Tyr Ile Ile Lys Glu
485 490 495

Gly Lys Leu Ala Val Val Ala Asp Asp Gly Val Thr Gln Tyr Ala Leu
500 505 510

Leu Ser Ala Gly Ser Cys Phe Gly Glu Ile Ser Ile Leu Asn Ile Lys
515 520 525

Gly Ser Lys Met Gly Asn Arg Arg Thr Ala Asn Ile Arg Ser Leu Gly
530 535 540

Tyr Ser Asp Leu Phe Cys Leu Ser Lys Asp Asp Leu Met Glu Ala Val
545 550 555 560

Thr Glu Tyr Pro Asp Ala Lys Lys Val Leu Glu Glu Arg Gly Arg Glu
565 570 575

Ile Leu Met Lys Glu Gly Leu Leu Asp Glu Asn Glu Val Ala Thr Ser
580 585 590

Met Glu Val Asp Val Gln Glu Lys Leu Gly Gln Leu Glu Thr Asn Met
595 600 605

Glu Thr Leu Tyr Thr Arg Phe Gly Arg Leu Leu Ala Glu Tyr Thr Gly
610 615 620

Ala Gln Gln Lys Leu Lys Gln Arg Ile Thr Val Leu Glu Thr Lys Met
625 630 635 640

Lys Gln Asn Asn Glu Asp Asp Tyr Leu Ser Asp Gly Met Asn Ser Pro
645 650 655

Glu Leu Ala Ala Ala Asp Glu Pro
660

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
100
101
102
103
104
105
106
107
108
109
110
111
112
113
114
115
116
117
118
119
120
121
122
123
124
125
126
127
128
129
130
131
132
133
134
135
136
137
138
139
140
141
142
143
144
145
146
147
148
149
150
151
152
153
154
155
156
157
158
159
160
161
162
163
164
165
166
167
168
169
170
171
172
173
174
175
176
177
178
179
180
181
182
183
184
185
186
187
188
189
190
191
192
193
194
195
196
197
198
199
200
201
202
203
204
205
206
207
208
209
210
211
212
213
214
215
216
217
218
219
220
221
222
223
224
225
226
227
228
229
230
231
232
233
234
235
236
237
238
239
240
241
242
243
244
245
246
247
248
249
250
251
252
253
254
255
256
257
258
259
260
261
262
263
264
265
266
267
268
269
270
271
272
273
274
275
276
277
278
279
280
281
282
283
284
285
286
287
288
289
290
291
292
293
294
295
296
297
298
299
300
301
302
303
304
305
306
307
308
309
310
311
312
313
314
315
316
317
318
319
320
321
322
323
324
325
326
327
328
329
330
331
332
333
334
335
336
337
338
339
340
341
342
343
344
345
346
347
348
349
350
351
352
353
354
355
356
357
358
359
360
361
362
363
364
365
366
367
368
369
370
371
372
373
374
375
376
377
378
379
380
381
382
383
384
385
386
387
388
389
390
391
392
393
394
395
396
397
398
399
400
401
402
403
404
405
406
407
408
409
410
411
412
413
414
415
416
417
418
419
420
421
422
423
424
425
426
427
428
429
430
431
432
433
434
435
436
437
438
439
440
441
442
443
444
445
446
447
448
449
450
451
452
453
454
455
456
457
458
459
460
461
462
463
464
465
466
467
468
469
470
471
472
473
474
475
476
477
478
479
480
481
482
483
484
485
486
487
488
489
490
491
492
493
494
495
496
497
498
499
500
501
502
503
504
505
506
507
508
509
510
511
512
513
514
515
516
517
518
519
520
521
522
523
524
525
526
527
528
529
530
531
532
533
534
535
536
537
538
539
540
541
542
543
544
545
546
547
548
549
550
551
552
553
554
555
556
557
558
559
560
561
562
563
564
565
566
567
568
569
570
571
572
573
574
575
576
577
578
579
580
581
582
583
584
585
586
587
588
589
590
591
592
593
594
595
596
597
598
599
600
601
602
603
604
605
606
607
608
609
610
611
612
613
614
615
616
617
618
619
620
621
622
623
624
625
626
627
628
629
630
631
632
633
634
635
636
637
638
639
640
641
642
643
644
645
646
647
648
649
650
651
652
653
654
655
656
657
658
659
660
661
662
663
664
665
666
667
668
669
670
671
672
673
674
675
676
677
678
679
680
681
682
683
684
685
686
687
688
689
690
691
692
693
694
695
696
697
698
699
700
701
702
703
704
705
706
707
708
709
710
711
712
713
714
715
716
717
718
719
720
721
722
723
724
725
726
727
728
729
730
731
732
733
734
735
736
737
738
739
740
741
742
743
744
745
746
747
748
749
750
751
752
753
754
755
756
757
758
759
760
761
762
763
764
765
766
767
768
769
770
771
772
773
774
775
776
777
778
779
780
781
782
783
784
785
786
787
788
789
790
791
792
793
794
795
796
797
798
799
800
801
802
803
804
805
806
807
808
809
810
811
812
813
814
815
816
817
818
819
820
821
822
823
824
825
826
827
828
829
830
831
832
833
834
835
836
837
838
839
840
841
842
843
844
845
846
847
848
849
850
851
852
853
854
855
856
857
858
859
860
861
862
863
864
865
866
867
868
869
870
871
872
873
874
875
876
877
878
879
880
881
882
883
884
885
886
887
888
889
890
891
892
893
894
895
896
897
898
899
900
901
902
903
904
905
906
907
908
909
910
911
912
913
914
915
916
917
918
919
920
921
922
923
924
925
926
927
928
929
930
931
932
933
934
935
936
937
938
939
940
941
942
943
944
945
946
947
948
949
950
951
952
953
954
955
956
957
958
959
960
961
962
963
964
965
966
967
968
969
970
971
972
973
974
975
976
977
978
979
980
981
982
983
984
985
986
987
988
989
990
991
992
993
994
995
996
997
998
999
1000
1001
1002
1003
1004
1005
1006
1007
1008
1009
1010
1011
1012
1013
1014
1015
1016
1017
1018
1019
1020
1021
1022
1023
1024
1025
1026
1027
1028
1029
1030
1031
1032
1033
1034
1035
1036
1037
1038
1039
1040
1041
1042
1043
1044
1045
1046
1047
1048
1049
1050
1051
1052
1053
1054
1055
1056
1057
1058
1059
1060
1061
1062
1063
1064
1065
1066
1067
1068
1069
1070
1071
1072
1073
1074
1075
1076
1077
1078
1079
1080
1081
1082
1083
1084
1085
1086
1087
1088
1089
1090
1091
1092
1093
1094
1095
1096
1097
1098
1099
1100
1101
1102
1103
1104
1105
1106
1107
1108
1109
1110
1111
1112
1113
1114
1115
1116
1117
1118
1119
1120
1121
1122
1123
1124
1125
1126
1127
1128
1129
1130
1131
1132
1133
1134
1135
1136
1137
1138
1139
1140
1141
1142
1143
1144
1145
1146
1147
1148
1149
1150
1151
1152
1153
1154
1155
1156
1157
1158
1159
1160
1161
1162
1163
1164
1165
1166
1167
1168
1169
1170
1171
1172
1173
1174
1175
1176
1177
1178
1179
1180
1181
1182
1183
1184
1185
1186
1187
1188
1189
1190
1191
1192
1193
1194
1195
1196
1197
1198
1199
1200
1201
1202
1203
1204
1205
1206
1207
1208
1209
1210
1211
1212
1213
1214
1215
1216
1217
1218
1219
1220
1221
1222
1223
1224
1225
1226
1227
1228
1229
1230
1231
1232
1233
1234
1235
1236
1237
1238
1239
1240
1241
1242
1243
1244
1245
1246
1247
1248
1249
1250
1251
1252
1253
1254
1255
1256
1257
1258
1259
1260
1261
1262
1263
1264
1265
1266
1267
1268
1269
1270
1271
1272
1273
1274
1275
1276
1277
1278
1279
1280
1281
1282
1283
1284
1285
1286
1287
1288
1289
1290
1291
1292
1293
1294
1295
1296
1297
1298
1299
1300
1301
1302
1303
1304
1305
1306
1307
1308
1309
1310
1311
1312
1313
1314
1315
1316
1317
1318
1319
1320
1321
1322
1323
1324
1325
1326
1327
1328
1329
1330
1331
1332
1333
1334
1335
1336
1337
1338
1339
1340
1341
1342
1343
1344
1345
1346
1347
1348
1349
1350
1351
1352
1353
1354
1355
1356
1357
1358
1359
1360
1361
1362
1363
1364
1365
1366
1367
1368
1369
1370
1371
1372
1373
1374
1375
1376
1377
1378
1379
1380
1381
1382
1383
1384
1385
1386
1387
1388
1389
1390
1391
1392
1393
1394
1395
1396
1397
1398
1399
1400
1401
1402
1403
1404
1405
1406
1407
1408
1409
1410
1411
1412
1413
1414
1415
1416
1417
1418
1419
1420
1421
1422
1423
1424
1425
1426
1427
1428
1429
1430
1431
1432
1433
1434
1435
1436
1437
1438
1439
1440
1441
1442
1443
1444
1445
1446
1447
1448
1449
1450
1451
1452
1453
1454
1455
1456
1457
1458
1459
1460
1461
1462
1463
1464
1465
1466
1467
1468
1469
1470
1471
1472
1473
1474
1475
1476
1477
1478
1479
1480
1481
1482
1483
1484
1485
1486
1487
1488
1489
1490
1491
1492
1493
1494
1495
1496
1497
1498
1499
1500
1501
1502
1503
1504
1505
1506
1507
1508
1509
1510
1511
1512
1513
1514
1515
1516
1517
1518
1519
1520
1521
1522
1523
1524
1525
1526
1527
1528
1529
1530
1531
1532
1533
1534
1535
1536
1537
1538
1539
1540
1541
1542
1543
1544
1545
1546
1547
1548
1549
1550
1551
1552
1553
1554
1555
1556
1557
1558
1559
1560
1561
1562
1563
1564
1565
1566
1567
1568
1569
1570
1571
1572
1573
1574
1575
1576
1577
1578
1579
1580
1581
1582
1583
1584
1585
1586
1587
1588
1589
1590
1591
1592
1593
1594
1595
1596
1597
1598
1599
1600
1601
1602
1603
1604
1605
1606
1607
1608
1609
1610
1611
1612
1613
1614
1615
1616
1617
1618
1619
1620
1621
1622
1623
1624
1625
1626
1627
1628
1629
1630
1631
1632
1633
1634
1635
1636
1637
1638
1639
1640
1641
1642
1643
1644
1645
1646
1647
1648
1649
1650
1651
1652
1653
1654
1655
1656
1657
1658
1659
1660
1661
1662
1663
1664
1665
1666
1667
1668
1669
1670
1671
1672
1673
1674
1675
1676
1677
1678
1679
1680
1681
1682
1683
1684
1685
1686
1687
1688
1689
1690
1691
1692
1693
1694
1695
1696
1697
1698
1699
1700
1701
1702
1703
1704
1705
1706
1707
1708
1709
1710
1711
1712
1713
1714
1715
1716
1717
1718
1719
1720
1721
1722
1723
1724
1725
1726
1727
1728
1729
1730
1731
1732
1733
1734
1735
1736
1737
1738
1739
1740
1741
1742
1743
1744
1745
1746
1747
1748
1749
1750
1751
1752
1753
1754
1755
1756
1757
1758
1759
1760
1761
1762
1763
1764
1765
1766
1767
1768
1769
1770
1771
1772
1773
1774
1775
1776
1777
1778
1779
1780
1781
1782
1783
1784
1785
1786
1787
1788
1789
1790
1791
1792
1793
1794
1795
1796
1797
1798
1799
1800
1801
1802
1803
1804
1805
1806
1807
1808
1809
1810
1811
1812
1813
1814
1815
1816
1817
1818
1819
1820
1821
1822
1823
1824
1825
1826
1827
1828
1829
1830
1831
1832
1833
1834
1835
1836
1837
1838
1839
1840
1841
1842
1843
1844
1845
1846
1847
1848
1849
1850
1851
1852
1853
1854
1855
1856
1857
1858
1859
1860
1861
1862
1863
1864
1865
1866
1867
1868
1869
1870
1871
1872
1873
1874
1875
1876
1877
1878
1879
1880
1881
1882
1883
1884
1885
1886
1887
1888
1889
1890
1891
1892
1893
1894
1895
1896
1897
1898
1899
1900
1901
1902
1903
1904
1905
1906
1907
1908
1909
1910
1911
1912
1913
1914
1915
1916
1917
1918
1919
1920
1921
1922
1923
1924
1925
1926
1927
1928
1929
1930
1931
1932
1933
1934
1935
1936
1937
1938
1939
1940
1941
1942
1943
1944
1945
1946
1947
1948
1949
1950
1951
1952
1953
1954
1955
1956
1957
1958
1959
1960
1961
1962
1963
1964
1965
1966
1967
1968
1969
1970
1971
1972
1973
1974
1975
1976
1977
1978
1979
1980
1981
1982
1983
1984
1985
1986
1987
1988
1989
1990
1991
1992
1993
1994
1995
1996
1997
1998
1999
2000
2001
2002
2003
2004
2005
2006
2007
2008
2009
2010
2011
2012
2013
2014
2015
2016
2017
2018
2019
2020
2021
2022
2023
2024
2025
2026
2027
2028
2029
2030
2031
2032
2033
2034
2035
2036
2037
2038
2039
2040
2041
2042
2043
2044
2045
2046
2047
2048
2049
2050
2051
2052
2053
2054
2055
2056
2057
2058
2059
2060
2061
2062
2063
2064
2065
2066
2067
2068
2069
2070
2071
2072
2073
2074
2075
2076
2077
2078
2079
2080
2081
2082
2083
2084
2085
2086
2087
2088
2089
2090
2091
2092
2093
2094
2095
2096
2097
2098
2099
2100
2101
2102
2103
2104
2105
2106
2107
2108
2109
2110
2111
2112
2113
2114
2115
2116
2117
2118
2119
2120
2121
2122
2123
2124
2125
2126
2127
2128
2129
2130
2131
2132
2133
2134
2135
2136
2137
2138
2139
2140
2141
2142
2143
2144
2145
2146
2147
2148
2149
2150
2151
2152
2153
2154
2155
2156
2157
2158
2159
2160
2161
2162
2163
2164
2165
2166
2167
2168
2169
2170
2171
2172
2173
2174
2175
2176
2177
2178
2179
2180
2181
2182
2183
2184
2185
2186

<220>
 <223> Primer
 <400> 6
 agagcctgct tcagtga 17

<210> 7
 <211> 17
 <212> DNA
 <213> artificial

<220>
 <223> Primer
 <400> 7
 tcactgaagc aggctct 17

<210> 8
 <211> 17
 <212> DNA
 <213> artificial
 <220>
 <223> Primer
 <400> 8
 ttactggtcc acactga 17

<210> 9
 <211> 17
 <212> DNA
 <213> artificial
 <220>
 <223> Primer
 <400> 9
 tcagtgtgga ccagtaa 17

<210> 10
 <211> 20
 <212> DNA
 <213> artificial
 <220>
 <223> Primer
 <400> 10
 acgcacagct aatatccgca 20

<210> 11
 <211> 20
 <212> DNA
 <213> artificial

<220>
 <223> Primer
 <400> 11
 tgcggatatt agctgtgcgt 20

<210> 12
 <211> 21
 <212> DNA
 <213> artificial

<220>
 <223> Primer
 <400> 12
 tcagagaatg ggccaacaag a 21

<210> 13
 <211> 20
 <212> DNA
 <213> artificial

<220>
 <223> Primer

<400> 13
 cgaaaacgct cgaggaatga 20

<210> 14
 <211> 26
 <212> DNA
 <213> artificial

<220>
 <223> Primer/Probe

<400> 14
 caggcctagg ttctctctct cgaaa 26

<210> 15
 <211> 732
 <212> PRT
 <213> Oryctolagus cuniculus

<400> 15

Met Ser Ser Trp Arg Ser Cys Ala Arg Ala Pro Leu Ser Gly Ser Ala
 1 5 10 15

Trp Arg Arg Ser Ala Ala Thr Arg Arg Ser Arg Arg Cys Leu Lys Thr
 20 25 30

Lys Arg Lys Arg Trp Ser Ser Gly Lys Gly Thr Pro Met Gln Ser Thr
 35 40 45

Gln Cys Glu Thr Arg Arg Arg Ala Gln Thr Pro Cys Glu Ser Thr Gly
 50 55 60

His Thr Trp Arg Met Thr Glu Lys Ser Asn Gly Val Lys Ser Ser Pro
 65 70 75 80
 Ala Asn Asn His Asn Asn His Val Pro Ala Thr Ile Lys Ala Asn Gly
 85 90 95
 Lys Asp Glu Ser Arg Thr Arg Ser Arg Pro Gln Ser Ala Ala Asp Asp
 100 105 110
 Asp Thr Ser Ser Glu Leu Gln Arg Leu Ala Glu Met Asp Ala Pro Gln
 115 120 125
 Gln Arg Arg Gly Gly Phe Arg Arg Ile Val Arg Leu Val Gly Val Ile
 130 135 140
 Arg Gln Trp Ala Asn Arg Asn Phe Arg Glu Glu Glu Ala Arg Pro Asp
 145 150 155 160
 Ser Phe Leu Glu Arg Phe Arg Gly Pro Glu Leu Gln Thr Val Thr Thr
 165 170 175
 Gln Gln Gly Asp Gly Lys Gly Asp Lys Asp Gly Asp Gly Lys Gly Thr
 180 185 190
 Lys Lys Lys Phe Glu Leu Phe Val Leu Asp Pro Ala Gly Asp Trp Tyr
 195 200 205
 Tyr Arg Trp Leu Phe Val Ile Ala Met Pro Val Leu Tyr Asn Trp Cys
 210 215 220
 Leu Leu Val Ala Arg Ala Cys Phe Ser Asp Leu Gln Arg Gly Tyr Phe
 225 230 235 240
 Leu Val Trp Leu Val Leu Asp Tyr Phe Ser Asp Val Val Tyr Ile Ala
 245 250 255
 Asp Leu Phe Ile Arg Leu Arg Thr Gly Phe Leu Glu Gln Gly Leu Leu
 260 265 270
 Val Lys Asp Pro Lys Lys Leu Arg Asp Asn Tyr Ile His Thr Leu Gln
 275 280 285
 Phe Lys Leu Asp Val Ala Ser Ile Ile Pro Thr Asp Leu Ile Tyr Phe
 290 295 300
 Ala Val Gly Ile His Asn Pro Glu Leu Arg Phe Asn Arg Leu Leu His
 305 310 315 320
 Phe Ala Arg Met Phe Glu Phe Phe Asp Arg Thr Glu Thr Arg Thr Ser
 325 330 335
 Tyr Pro Asn Ile Phe Arg Ile Ser Asn Leu Val Leu Tyr Ile Leu Val
 340 345 350
 Ile Ile His Trp Asn Ala Cys Ile Tyr Tyr Ala Ile Ser Lys Ser Ile
 355 360 365
 Gly Phe Gly Val Asp Thr Trp Val Tyr Pro Asn Ile Thr Asp Pro Glu
 370 375 380

Tyr Gly Tyr Leu Ala Arg Glu Tyr Ile Tyr Cys Leu Tyr Trp Ser Thr
 385 390 395 400
 Leu Thr Leu Thr Thr Ile Gly Glu Thr Pro Pro Val Lys Asp Glu
 405 410 415
 Glu Tyr Leu Phe Val Ile Phe Asp Phe Leu Ile Gly Val Leu Ile Phe
 420 425 430
 Ala Thr Ile Val Gly Asn Val Gly Ser Met Ile Ser Asn Met Asn Ala
 435 440 445
 Thr Arg Ala Glu Phe Gln Ala Lys Ile Asp Ala Val Lys His Tyr Met
 450 455 460
 Gln Phe Arg Lys Val Ser Lys Glu Met Glu Ala Lys Val Ile Lys Trp
 465 470 475 480
 Phe Asp Tyr Leu Trp Thr Asn Lys Lys Thr Val Asp Glu Arg Glu Val
 485 490 495
 Leu Lys Asn Leu Pro Ala Lys Leu Arg Ala Glu Ile Ala Ile Asn Val
 500 505 510
 His Leu Ser Thr Leu Lys Lys Val Arg Ile Phe Gln Asp Cys Glu Ala
 515 520 525
 Gly Leu Leu Val Glu Leu Val Leu Lys Leu Arg Pro Gln Val Phe Ser
 530 535 540
 Pro Gly Asp Tyr Ile Cys Arg Lys Gly Asp Ile Gly Lys Glu Met Tyr
 545 550 555 560
 Ile Ile Lys Glu Gly Lys Leu Ala Val Val Ala Asp Asp Gly Val Thr
 565 570 575
 Gln Tyr Ala Leu Leu Ser Ala Gly Ser Cys Phe Gly Glu Ile Ser Ile
 580 585 590
 Leu Asn Ile Lys Gly Ser Lys Met Gly Asn Arg Arg Thr Ala Asn Ile
 595 600 605
 Arg Ser Leu Gly Tyr Ser Asp Leu Phe Cys Leu Ser Lys Asp Asp Leu
 610 615 620
 Met Glu Ala Val Thr Glu Tyr Pro Asp Ala Lys Lys Val Leu Glu Glu
 625 630 635 640
 Arg Gly Arg Glu Ile Leu Met Lys Glu Gly Leu Leu Asp Glu Asn Glu
 645 650 655
 Val Ala Ala Ser Met Glu Val Asp Val Gln Glu Lys Leu Lys Gln Leu
 660 665 670
 Glu Thr Asn Met Glu Thr Leu Tyr Thr Arg Phe Gly Arg Leu Leu Ala
 675 680 685
 Glu Tyr Thr Gly Ala Gln Gln Lys Leu Lys Gln Arg Ile Thr Val Leu
 690 695 700
 Glu Val Lys Met Lys Gln Asn Thr Glu Asp Asp Tyr Leu Ser Asp Gly

705 710 715 720

Met Asn Ser Pro Glu Pro Ala Ala Ala Glu Gln Pro
725 730

<210> 16
<211> 663
<212> PRT
<213> Bos taurus

<400> 16

Met Thr Glu Lys Ala Asn Gly Val Lys Ser Ser Pro Ala Asn Asn His
1 5 10 15

Asn His His Ala Pro Pro Ala Ile Lys Ala Ser Gly Lys Asp Asp His
20 25 30

Arg Ala Ser Ser Arg Pro Gln Ser Ala Ala Ala Asp Asp Thr Ser Ser
35 40 45

Glu Leu Gln Gln Leu Ala Glu Met Asp Ala Pro Gln Gln Arg Arg Gly
50 55 60

Gly Phe Arg Arg Ile Ala Arg Leu Val Gly Val Leu Arg Glu Trp Ala
65 70 75 80

Tyr Arg Asn Phe Arg Glu Glu Glu Pro Arg Pro Asp Ser Phe Leu Glu
85 90 95

Arg Phe Arg Gly Pro Glu Leu His Thr Val Thr Thr Gln Gln Gly Asp
100 105 110

Gly Lys Gly Asp Lys Asp Gly Glu Gly Lys Gly Thr Lys Lys Lys Phe
115 120 125

Glu Leu Phe Val Leu Asp Pro Ala Gly Asp Trp Tyr Tyr Arg Trp Leu
130 135 140

Phe Leu Ile Ala Leu Pro Val Leu Tyr Asn Trp Cys Leu Leu Val Ala
145 150 155 160

Arg Ala Cys Phe Ser Asp Leu Gln Lys Gly Tyr Tyr Ile Val Trp Leu
165 170 175

Val Leu Asp Tyr Val Ser Asp Val Val Tyr Ile Ala Asp Leu Phe Ile
180 185 190

Arg Leu Arg Thr Gly Phe Leu Glu Gln Gly Leu Leu Val Lys Asp Thr
195 200 205

Lys Lys Leu Arg Asp Asn Tyr Ile His Thr Met Gln Phe Lys Leu Asp
210 215 220

Val Ala Ser Ile Ile Pro Thr Asp Leu Ile Tyr Phe Ala Val Gly Ile
225 230 235 240

His Asn Pro Glu Val Arg Phe Asn Arg Leu Leu His Phe Ala Arg Met
245 250 255

Phe Glu Phe Phe Asp Arg Thr Glu Thr Arg Thr Ser Tyr Pro Asn Ile

260										265										270										
Phe	Arg	Ile	Ser	Asn	Leu	Ile	Leu	Tyr	Ile	Leu	Ile	Ile	Ile	His	Trp															
	275						280					285																		
Asn	Ala	Cys	Ile	Tyr	Tyr	Ala	Ile	Ser	Lys	Ser	Ile	Gly	Phe	Gly	Val															
	290					295					300																			
Asp	Thr	Trp	Val	Tyr	Pro	Asn	Ile	Thr	Asp	Pro	Glu	Tyr	Gly	Tyr	Leu															
	305				310					315					320															
Ser	Arg	Glu	Tyr	Ile	Tyr	Cys	Leu	Tyr	Trp	Ser	Thr	Leu	Thr	Leu	Thr															
			325						330					335																
Thr	Ile	Gly	Glu	Thr	Pro	Pro	Pro	Val	Lys	Asp	Glu	Glu	Tyr	Leu	Phe															
			340					345					350																	
Val	Ile	Phe	Asp	Phe	Leu	Ile	Gly	Val	Leu	Ile	Phe	Ala	Thr	Ile	Val															
		355					360					365																		
Gly	Asn	Val	Gly	Ser	Met	Ile	Ser	Asn	Met	Asn	Ala	Thr	Arg	Ala	Glu															
	370				375					380																				
Phe	Gln	Ala	Lys	Ile	Asp	Ala	Val	Lys	His	Tyr	Met	Gln	Phe	Arg	Lys															
	385				390					395					400															
Val	Ser	Lys	Glu	Met	Glu	Ala	Lys	Val	Ile	Arg	Trp	Phe	Asp	Tyr	Leu															
			405						410					415																
Trp	Thr	Asn	Lys	Lys	Ser	Val	Asp	Glu	Arg	Glu	Val	Leu	Lys	Asn	Leu															
		420					425					430																		
Pro	Ala	Lys	Leu	Arg	Ala	Glu	Ile	Ala	Ile	Asn	Val	His	Leu	Ser	Thr															
	435					440						445																		
Leu	Lys	Lys	Val	Arg	Ile	Phe	Gln	Asp	Cys	Glu	Ala	Gly	Leu	Leu	Val															
	450				455					460																				
Glu	Leu	Val	Leu	Lys	Leu	Arg	Pro	Gln	Val	Phe	Ser	Pro	Gly	Asp	Tyr															
	465				470				475					480																
Ile	Cys	Arg	Lys	Gly	Asp	Ile	Gly	Lys	Glu	Met	Tyr	Ile	Ile	Lys	Glu															
		485						490						495																
Gly	Lys	Leu	Ala	Val	Val	Ala	Asp	Asp	Gly	Val	Thr	Gln	Tyr	Ala	Leu															
		500					505						510																	
Leu	Ser	Ala	Gly	Ser	Cys	Phe	Gly	Glu	Ile	Ser	Ile	Leu	Asn	Ile	Lys															
	515					520						525																		
Gly	Ser	Lys	Met	Gly	Asn	Arg	Arg	Thr	Ala	Asn	Ile	Arg	Ser	Leu	Gly															
	530				535						540																			
Tyr	Ser	Asp	Leu	Phe	Cys	Leu	Ser	Lys	Asp	Asp	Leu	Met	Glu	Ala	Val															
	545				550				555					560																
Thr	Glu	Tyr	Pro	Asp	Ala	Lys	Arg	Val	Leu	Glu	Glu	Arg	Gly	Arg	Glu															
		565						570					575																	
Ile	Leu	Met	Lys	Glu	Gly	Leu	Leu	Asp	Glu	Asn	Glu	Val	Ala	Ala	Ser															
		580					585						590																	

Met Glu Val Asp Val Gln Glu Lys Leu Glu Gln Leu Glu Thr Asn Met
595 600 605

Asp Thr Leu Tyr Thr Arg Phe Ala Arg Leu Leu Ala Glu Tyr Thr Gly
610 615 620

Ala Gln Gln Lys Leu Lys Gln Arg Ile Thr Val Leu Glu Thr Lys Met
625 630 635 640

Lys Gln Asn Asn Glu Asp Asp Ser Leu Ser Asp Gly Met Asn Ser Pro
645 650 655

Glu Pro Pro Ala Glu Lys Pro
660

<210> 17
<211> 664
<212> PRT
<213> Mus musculus

<400> 17

Met Met Thr Glu Lys Ser Asn Gly Val Lys Ser Ser Pro Ala Asn Asn
1 5 10 15

His Asn His His Pro Pro Pro Ser Ile Lys Ala Asn Gly Lys Asp Asp
20 25 30

His Arg Ala Gly Ser Arg Pro Gln Ser Val Ala Ala Asp Asp Asp Thr
35 40 45

Ser Ser Glu Leu Gln Arg Leu Ala Glu Met Asp Thr Pro Arg Arg Gly
50 55 60

Arg Gly Gly Phe Arg Arg Ile Val Arg Leu Val Gly Ile Ile Arg Asp
65 70 75 80

Trp Ala Asn Lys Asn Phe Arg Glu Glu Glu Pro Arg Pro Asp Ser Phe
85 90 95

Leu Glu Arg Phe Arg Gly Pro Glu Leu Gln Thr Val Thr Pro His Gln
100 105 110

Gly Asp Gly Lys Gly Asp Lys Asp Gly Glu Gly Lys Gly Thr Lys Lys
115 120 125

Lys Phe Glu Leu Phe Val Leu Asp Pro Ala Gly Asp Trp Tyr Tyr Arg
130 135 140

Trp Leu Phe Val Ile Ala Met Pro Val Leu Tyr Asn Trp Cys Leu Leu
145 150 155 160

Val Ala Arg Ala Cys Phe Ser Asp Leu Gln Arg Asn Tyr Phe Val Val
165 170 175

Trp Leu Val Leu Asp Tyr Phe Ser Asp Thr Val Tyr Ile Ala Asp Leu
180 185 190

Ile Ile Arg Leu Arg Thr Gly Phe Leu Glu Gln Gly Leu Leu Val Lys
195 200 205

Asp Pro Lys Lys Leu Arg Asp Asn Tyr Ile His Thr Leu Gln Phe Lys
 210 215 220
 Leu Asp Val Ala Ser Ile Ile Pro Thr Asp Leu Ile Tyr Phe Ala Val
 225 230 235 240
 Gly Ile His Ser Pro Glu Val Arg Phe Asn Arg Leu Leu His Phe Ala
 245 250 255
 Arg Met Phe Glu Phe Phe Asp Arg Thr Glu Thr Arg Thr Ser Tyr Pro
 260 265 270
 Asn Ile Phe Arg Ile Ser Asn Leu Val Leu Tyr Ile Leu Val Ile Ile
 275 280 285
 His Trp Asn Ala Cys Ile Tyr Tyr Ala Ile Ser Lys Ser Ile Gly Phe
 290 295 300
 Gly Val Asp Thr Trp Val Tyr Pro Asn Ile Thr Asp Pro Glu Tyr Gly
 305 310 315 320
 Tyr Leu Ala Arg Glu Tyr Ile Tyr Cys Leu Tyr Trp Ser Thr Leu Thr
 325 330 335
 Leu Thr Thr Ile Gly Glu Thr Pro Pro Val Lys Asp Glu Tyr
 340 345 350
 Leu Phe Phe Ile Phe Asp Phe Leu Ile Gly Val Leu Ile Phe Ala Thr
 355 360 365
 Ile Val Gly Asn Val Gly Ser Met Ile Ser Asn Met Asn Ala Thr Arg
 370 375 380
 Ala Glu Phe Gln Ala Lys Ile Asp Ala Val Lys His Tyr Met Gln Phe
 385 390 395 400
 Arg Lys Val Ser Lys Asp Met Glu Ala Lys Val Ile Lys Trp Phe Asp
 405 410 415
 Tyr Leu Trp Thr Asn Lys Lys Thr Val Asp Glu Arg Glu Val Leu Lys
 420 425 430
 Asn Leu Pro Ala Lys Leu Arg Ala Glu Ile Ala Ile Asn Val His Leu
 435 440 445
 Ser Thr Leu Lys Lys Val Arg Ile Phe Gln Asp Cys Glu Ala Gly Leu
 450 455 460
 Leu Val Glu Leu Val Leu Lys Leu Arg Pro Gln Val Phe Ser Pro Gly
 465 470 475 480
 Asp Tyr Ile Cys Arg Lys Gly Asp Ile Gly Lys Glu Met Tyr Ile Ile
 485 490 495
 Lys Glu Gly Lys Leu Ala Val Val Ala Asp Asp Gly Val Thr Gln Tyr
 500 505 510
 Ala Leu Leu Ser Ala Gly Ser Cys Phe Gly Glu Ile Ser Ile Leu Asn
 515 520 525

Ile Lys Gly Ser Lys Met Gly Asn Arg Arg Thr Gly Thr Ile Arg Ser
530 535 540

Leu Gly Tyr Ser Asp Leu Phe Cys Leu Ser Lys Asp Asp Leu Met Glu
545 550 555 560

Ala Val Thr Glu Tyr Pro Asp Ala Lys Lys Val Leu Glu Glu Arg Gly
565 570 575

Arg Glu Ile Leu Met Lys Glu Gly Leu Leu Asp Glu Asn Glu Val Ala
580 585 590

Ala Ser Met Glu Val Asp Val Gln Glu Lys Leu Glu Gln Leu Glu Thr
595 600 605

Asn Met Glu Thr Leu Tyr Thr Arg Phe Ala Arg Leu Leu Ala Glu Tyr
610 615 620

Thr Gly Ala Gln Gln Lys Leu Lys Gln Arg Ile Thr Val Leu Glu Thr
625 630 635 640

Lys Met Lys Gln Asn His Glu Asp Asp Tyr Leu Ser Asp Gly Ile Asn
645 650 655

Thr Pro Glu Pro Ala Val Ala Glu
660

<210> 18

<211> 664

<212> PRT

<213> Rattus norvegicus

<400> 18

Met Met Thr Glu Lys Ser Asn Gly Val Lys Ser Ser Pro Ala Asn Asn
1 5 10 15

His Asn His His Pro Pro Pro Ser Ile Lys Ala Asn Gly Lys Asp Asp
20 25 30

His Arg Ala Gly Ser Arg Pro Gln Ser Val Ala Ala Asp Asp Thr
35 40 45

Ser Pro Glu Leu Gln Arg Leu Ala Glu Met Asp Thr Pro Arg Arg Gly
50 55 60

Arg Gly Gly Phe Gln Arg Ile Val Arg Leu Val Gly Val Ile Arg Asp
65 70 75 80

Trp Ala Asn Lys Asn Phe Arg Glu Glu Glu Pro Arg Pro Asp Ser Phe
85 90 95

Leu Glu Arg Phe Arg Gly Pro Glu Leu Gln Thr Val Thr Thr His Gln
100 105 110

Gly Asp Asp Lys Gly Gly Lys Asp Gly Glu Gly Lys Gly Thr Lys Lys
115 120 125

Lys Phe Glu Leu Phe Val Leu Asp Pro Ala Gly Asp Trp Tyr Tyr Arg
130 135 140

Trp Leu Phe Val Ile Ala Met Pro Val Leu Tyr Asn Trp Cys Leu Leu
 145 150 155 160
 Val Ala Arg Ala Cys Phe Ser Asp Leu Gln Arg Asn Tyr Phe Val Val
 165 170 175
 Trp Leu Val Leu Asp Tyr Phe Ser Asp Thr Val Tyr Ile Ala Asp Leu
 180 185 190
 Ile Ile Arg Leu Arg Thr Gly Phe Leu Glu Gln Gly Leu Leu Val Lys
 195 200 205
 Asp Pro Lys Lys Leu Arg Asp Asn Tyr Ile His Thr Leu Gln Phe Lys
 210 215 220
 Leu Asp Val Ala Ser Ile Ile Pro Thr Asp Leu Ile Tyr Phe Ala Val
 225 230 235 240
 Gly Ile His Ser Pro Glu Val Arg Phe Asn Arg Leu Leu His Phe Ala
 245 250 255
 Arg Met Phe Glu Phe Phe Asp Arg Thr Glu Thr Arg Thr Ser Tyr Pro
 260 265 270
 Asn Ile Phe Arg Ile Ser Asn Leu Val Leu Tyr Ile Leu Val Ile Ile
 275 280 285
 His Trp Asn Ala Cys Ile Tyr Tyr Val Ile Ser Lys Ser Ile Gly Phe
 290 295 300
 Gly Val Asp Thr Trp Val Tyr Pro Asn Ile Thr Asp Pro Glu Tyr Gly
 305 310 315 320
 Tyr Leu Ala Arg Glu Tyr Ile Tyr Cys Leu Tyr Trp Ser Thr Leu Thr
 325 330 335
 Leu Thr Thr Ile Gly Glu Thr Pro Pro Val Lys Asp Glu Glu Tyr
 340 345 350
 Leu Phe Val Ile Phe Asp Phe Leu Ile Gly Val Leu Ile Phe Ala Thr
 355 360 365
 Ile Val Gly Asn Val Gly Ser Met Ile Ser Asn Met Asn Ala Thr Arg
 370 375 380
 Ala Glu Phe Gln Ala Lys Ile Asp Ala Val Lys His Tyr Met Gln Phe
 385 390 395 400
 Arg Lys Val Ser Lys Asp Met Glu Ala Lys Val Ile Lys Trp Phe Asp
 405 410 415
 Tyr Leu Trp Thr Asn Lys Lys Thr Val Asp Glu Arg Glu Val Leu Lys
 420 425 430
 Asn Leu Pro Ala Lys Leu Arg Ala Glu Ile Ala Ile Asn Val His Leu
 435 440 445
 Ser Thr Leu Lys Lys Val Arg Ile Phe Gln Asp Cys Glu Ala Gly Leu
 450 455 460
 Leu Val Glu Leu Val Leu Lys Leu Arg Pro Gln Val Phe Ser Pro Gly

465 470 475 480
 Asp Tyr Ile Cys Arg Lys Gly Asp Ile Gly Lys Glu Met Tyr Ile Ile
 485 490 495
 Lys Glu Gly Lys Leu Ala Val Val Ala Asp Asp Gly Val Thr Gln Tyr
 500 505 510
 Ala Leu Leu Ser Ala Gly Ser Cys Phe Gly Glu Ile Ser Ile Leu Asn
 515 520 525
 Ile Lys Gly Ser Lys Met Gly Asn Arg Arg Thr Ala Asn Ile Arg Ser
 530 535 540
 Leu Gly Tyr Ser Asp Leu Phe Cys Leu Ser Lys Asp Asp Leu Met Glu
 545 550 555 560
 Ala Val Thr Glu Tyr Pro Asp Ala Lys Lys Val Leu Glu Glu Arg Gly
 565 570 575
 Arg Glu Ile Leu Met Lys Glu Gly Leu Leu Asp Glu Asn Glu Val Ala
 580 585 590
 Ala Ser Met Glu Val Asp Val Gln Glu Lys Leu Glu Gln Leu Glu Thr
 595 600 605
 Asn Met Asp Thr Leu Tyr Thr Arg Phe Ala Arg Leu Leu Ala Glu Tyr
 610 615 620
 Thr Gly Ala Gln Gln Lys Leu Lys Gln Arg Ile Thr Val Leu Glu Thr
 625 630 635 640
 Lys Met Lys Gln Asn His Glu Asp Asp Tyr Leu Ser Asp Gly Ile Asn
 645 650 655
 Thr Pro Glu Pro Thr Ala Ala Glu
 660

<210> 19
 <211> 39
 <212> DNA
 <213> Homo sapiens

<400> 19
 gcagcagcgc ccgctactac tgctggctat ttgtcattg

39

<210> 20
 <211> 36
 <212> DNA
 <213> Homo sapiens

<400> 20
 gcagcagtcg actggctcgt cagcagcagc cagctc

36

<210> 21
 <211> 38
 <212> DNA
 <213> Homo sapiens

<400> 21
gcagcagcgg ccgcatgacc gaaaaaacca atggtgtg 38

<210> 22
<211> 36
<212> DNA
<213> Homo sapiens

<400> 22
gcagcagtcg acgaagacct gaggacggag ttccag 36

<210> 23
<211> 2190
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (20)..(2011)

<400> 23
ctctagatgt acatggagg atg acc gaa aaa acc aat ggt gtg aag agc tcc 52
Met Thr Glu Lys Thr Asn Gly Val Lys Ser Ser
1 5 10

cca gcc aat aat cac aac cat cat gca cct cct gcc atc aag gcc aat 100
Pro Ala Asn Asn His Asn His His Ala Pro Pro Ala Ile Lys Ala Asn
15 20 25

ggc aaa gat gac cac agg aca agc agc agg cca cac tct gca gct gac 148
Gly Lys Asp Asp His Arg Thr Ser Ser Arg Pro His Ser Ala Ala Asp
30 35 40

gat gac acc tcc tca gaa ctg cag agg ctg gca gac gtg gat gcc cca 196
Asp Asp Thr Ser Ser Glu Leu Gln Arg Leu Ala Asp Val Asp Ala Pro
45 50 55

cag cag gga agg agt ggc ttc cgc agg ata gtt cgc ctg gtg ggg atc 244
Gln Gln Gly Arg Ser Gly Phe Arg Arg Ile Val Arg Leu Val Gly Ile
60 65 70 75

atc aga gaa tgg gcc aac aag aat ttc cga gag gag gaa cct agg cct 292
Ile Arg Glu Trp Ala Asn Lys Asn Phe Arg Glu Glu Glu Pro Arg Pro
80 85 90

gac tca ttc ctc gag cgt ttt cgt ggg cct gaa ctc cag act gtg acc 340
Asp Ser Phe Leu Glu Arg Phe Arg Gly Pro Glu Leu Gln Thr Val Thr
95 100 105

aca cag gag ggg gat ggc aaa ggc gac aag gat ggc gag gac aaa ggc 388
Thr Gln Glu Gly Asp Gly Lys Gly Asp Lys Asp Gly Glu Asp Lys Gly
110 115 120

acc aag aag aaa ttt gaa cta ttt gtc ttg gac cca gct ggg gat ttg 436
Thr Lys Lys Lys Phe Glu Leu Phe Val Leu Asp Pro Ala Gly Asp Leu
125 130 135

tac tac tgc tgg cta ttt gtc att gcc atg ccc gtc ctt tac aac tgg 484
Tyr Tyr Cys Trp Leu Phe Val Ile Ala Met Pro Val Leu Tyr Asn Trp

140		145		150		155	
tgc ctg ctg gtg gcc aga gcc tgc ttc agt gac cta cag aaa ggc tac	532						
Cys Leu Leu Val Ala Arg Ala Cys Phe Ser Asp Leu Gln Lys Gly Tyr							
160		165		170			
tac ctg gtg tgg ctg gtg ctg gat tat gtc tca gat gtg gtc tac att	580						
Tyr Leu Val Trp Leu Val Leu Asp Tyr Val Ser Asp Val Val Tyr Ile							
175		180		185			
gcg gac ctc ttc atc cga ttg cgc aca ggt ttc ctg gag cag ggg ctg	628						
Ala Asp Leu Phe Ile Arg Leu Arg Thr Gly Phe Leu Glu Gln Gly Leu							
190		195		200			
ctg gtc aaa gat acc aag aaa ctg cga gac aac tac atc cac acc ctg	676						
Leu Val Lys Asp Thr Lys Lys Leu Arg Asp Asn Tyr Ile His Thr Leu							
205		210		215			
cag ttc aag ctg gat gtg gct tcc atc atc ccc act gac ctg atc tat	724						
Gln Phe Lys Leu Asp Val Ala Ser Ile Ile Pro Thr Asp Leu Ile Tyr							
220		225		230		235	
ttt gct gtg gac atc cac agc cct gag gtg cgc ttc aac cgc ctg ctg	772						
Phe Ala Val Asp Ile His Ser Pro Glu Val Arg Phe Asn Arg Leu Leu							
240		245		250			
Cac ttt gcc cgc atg ttt gag ttc ttt gac cgg aca gag aca cgc acc	820						
His Phe Ala Arg Met Phe Glu Phe Phe Asp Arg Thr Glu Thr Arg Thr							
255		260		265			
aac tac cct aac atc ttc cgc atc agc aac ctt gtc ctc tac atc ttg	868						
Asn Tyr Pro Asn Ile Phe Arg Ile Ser Asn Leu Val Leu Tyr Ile Leu							
270		275		280			
gtc atc atc cac tgg aat gcc tgc atc tat tat gcc atc tcc aaa tcc	916						
Val Ile Ile His Trp Asn Ala Cys Ile Tyr Tyr Ala Ile Ser Lys Ser							
285		290		295			
ata ggc ttt ggg gtc gac acc tgg gtt tac cca aac atc act gac cct	964						
Ile Gly Phe Gly Val Asp Thr Trp Val Tyr Pro Asn Ile Thr Asp Pro							
300		305		310		315	
gag tat ggc tac ctg gct agg gaa tac atc tat tgc ctt tac tgg tcc	1012						
Glu Tyr Gly Tyr Leu Ala Arg Glu Tyr Ile Tyr Cys Leu Tyr Trp Ser							
320		325		330			
aca ctg act ctc act acc att ggg gag aca cca ccc cct gta aag gat	1060						
Thr Leu Thr Leu Thr Thr Ile Gly Glu Thr Pro Pro Pro Val Lys Asp							
335		340		345			
gag gag tac cta ttt gtc atc ttt gac ttc ctg att ggc gtc ctc atc	1108						
Glu Glu Tyr Leu Phe Val Ile Phe Asp Phe Leu Ile Gly Val Leu Ile							
350		355		360			
ttt gcc acc atc gtg gga aat gtg ggc tcc atg atc tcc aac atg aat	1156						
Phe Ala Thr Ile Val Gly Asn Val Gly Ser Met Ile Ser Asn Met Asn							
365		370		375			
gcc acc cgg gca gag ttc cag gct aag atc gat gcc gtg aaa cac tac	1204						
Ala Thr Arg Ala Glu Phe Gln Ala Lys Ile Asp Ala Val Lys His Tyr							
380		385		390		395	

atg cag ttc cga aag gtc agc aag ggg atg gaa gcc aag gtc att agg	1252
Met Gln Phe Arg Lys Val Ser Lys Gly Met Glu Ala Lys Val Ile Arg	
400 405 410	
tggttt gac tac ttgttg acc aat aag aag aca gtg gat gag cga gaa	1300
Trp Phe Asp Tyr Leu Trp Thr Asn Lys Lys Thr Val Asp Glu Arg Glu	
415 420 425	
attctc aag aat ctgcca gcc aag ctcagg gctgag ata gcc atc aat	1348
Ile Leu Lys Asn Leu Pro Ala Lys Leu Arg Ala Glu Ile Ala Ile Asn	
430 435 440	
gtccac ttgtcc acactc aagaaa gtgcgc atcttc cat gat tgt gag	1396
Val His Leu Ser Thr Leu Lys Lys Val Arg Ile Phe His Asp Cys Glu	
445 450 455	
gctggc ctgctg gtagag ctggtg ctgaaa ctc cgt cctcag gtc ttc	1444
Ala Gly Leu Leu Val Glu Leu Val Leu Lys Leu Arg Pro Gln Val Phe	
460 465 470 475	
agtcct ggg gat tacatt tgcgcg aaggg gac atc ggc aag gag atg	1492
Ser Pro Gly Asp Tyr Ile Cys Arg Lys Gly Asp Ile Gly Lys Glu Met	
480 485 490	
tacatc attaag gagggc aaaa ctggca gtggtg gctgat gat ggtgtg	1540
Tyr Ile Ile Lys Glu Gly Lys Leu Ala Val Val Ala Asp Asp Gly Val	
495 500 505	
actcag tatgct ctgctg tcggct ggagcg tgc ttt ggc gag atc agt	1588
Thr Gln Tyr Ala Leu Leu Ser Ala Gly Ser Cys Phe Gly Glu Ile Ser	
510 515 520	
atcctt aacatt aagggc agtaaa atgggc aatcga cgc aca gct aat	1636
Ile Leu Asn Ile Lys Gly Ser Lys Met Gly Asn Arg Arg Thr Ala Asn	
525 530 535	
atccgc agcctg ggctac tcagat ctc ttc tgc ttgtcc aag gat gat	1684
Ile Arg Ser Leu Gly Tyr Ser Asp Leu Phe Cys Leu Ser Lys Asp Asp	
540 545 550 555	
cttatg gaagct gtgact gagtac cctgat gcc aagaaa gtc cta gaa	1732
Leu Met Glu Ala Val Thr Glu Tyr Pro Asp Ala Lys Lys Val Leu Glu	
560 565 570	
gagagg ggtcgg gagatc ctc atg aag gag gga ctg ctg gat gag aac	1780
Glu Arg Gly Arg Glu Ile Leu Met Lys Glu Gly Leu Leu Asp Glu Asn	
575 580 585	
gaagtg gcaacc agcatg gaggtc gacgtg cag gag aagcta gggcag	1828
Glu Val Ala Thr Ser Met Glu Val Asp Val Gln Glu Lys Leu Gly Gln	
590 595 600	
ctggag accaac atggaa acc ttgtac actcgc ttt ggc cgc ctg ctg	1876
Leu Glu Thr Asn Met Glu Thr Leu Tyr Thr Arg Phe Gly Arg Leu Leu	
605 610 615	
gctgag tacacg ggggcc cagcag aagctc aagcag cgc atcaca gtt	1924
Ala Glu Tyr Thr Gly Ala Gln Gln Lys Leu Lys Gln Arg Ile Thr Val	
620 625 630 635	

ctg gaa acc aag atg aaa cag aac aat gaa gat gac tac ctg tct gat 1972
 Leu Glu Thr Lys Met Lys Gln Asn Asn Glu Asp Asp Tyr Leu Ser Asp
 640 645 650

ggg atg aac agc cct gag ctg gct gct gct gac gag cca taagacctgg 2021
 Gly Met Asn Ser Pro Glu Leu Ala Ala Ala Asp Glu Pro
 655 660

ggcccaactg cctctccagc attggccttg gccttgatcc cagaagctag aggagctatt 2081
 tagatctcgg gatttacatg cattaccctc atgttccttg aattctocca aaagcctctc 2141
 tgacctctggg tttttggcct aaacatccaa gattccgcct cggatccc 2190

<210> 24
 <211> 664
 <212> PRT
 <213> Homo sapiens

<400> 24

Met Thr Glu Lys Thr Asn Gly Val Lys Ser Ser Pro Ala Asn Asn His
 1 5 10 15

Asn His His Ala Pro Pro Ala Ile Lys Ala Asn Gly Lys Asp Asp His
 20 25 30

Arg Thr Ser Ser Arg Pro His Ser Ala Ala Asp Asp Asp Thr Ser Ser
 35 40 45

Glu Leu Gln Arg Leu Ala Asp Val Asp Ala Pro Gln Gln Gly Arg Ser
 50 55 60

Gly Phe Arg Arg Ile Val Arg Leu Val Gly Ile Ile Arg Glu Trp Ala
 65 70 75 80

Asn Lys Asn Phe Arg Glu Glu Glu Pro Arg Pro Asp Ser Phe Leu Glu
 85 90 95

Arg Phe Arg Gly Pro Glu Leu Gln Thr Val Thr Thr Gln Glu Gly Asp
 100 105 110

Gly Lys Gly Asp Lys Asp Gly Glu Asp Lys Gly Thr Lys Lys Lys Phe
 115 120 125

Glu Leu Phe Val Leu Asp Pro Ala Gly Asp Leu Tyr Tyr Cys Trp Leu
 130 135 140

Phe Val Ile Ala Met Pro Val Leu Tyr Asn Trp Cys Leu Leu Val Ala
 145 150 155 160

Arg Ala Cys Phe Ser Asp Leu Gln Lys Gly Tyr Tyr Leu Val Trp Leu
165 170 175

Val Leu Asp Tyr Val Ser Asp Val Val Tyr Ile Ala Asp Leu Phe Ile
180 185 190

Arg Leu Arg Thr Gly Phe Leu Glu Gln Gly Leu Leu Val Lys Asp Thr
195 200 205

Lys Lys Leu Arg Asp Asn Tyr Ile His Thr Leu Gln Phe Lys Leu Asp
210 215 220

Val Ala Ser Ile Ile Pro Thr Asp Leu Ile Tyr Phe Ala Val Asp Ile
225 230 235 240

His Ser Pro Glu Val Arg Phe Asn Arg Leu Leu His Phe Ala Arg Met
245 250 255

Phe Glu Phe Phe Asp Arg Thr Glu Thr Arg Thr Asn Tyr Pro Asn Ile
260 265 270

Phe Arg Ile Ser Asn Leu Val Leu Tyr Ile Leu Val Ile Ile His Trp
275 280 285

Asn Ala Cys Ile Tyr Tyr Ala Ile Ser Lys Ser Ile Gly Phe Gly Val
290 295 300

Asp Thr Trp Val Tyr Pro Asn Ile Thr Asp Pro Glu Tyr Gly Tyr Leu
305 310 315 320

Ala Arg Glu Tyr Ile Tyr Cys Leu Tyr Trp Ser Thr Leu Thr Leu Thr
325 330 335

Thr Ile Gly Glu Thr Pro Pro Pro Val Lys Asp Glu Glu Tyr Leu Phe
340 345 350

Val Ile Phe Asp Phe Leu Ile Gly Val Leu Ile Phe Ala Thr Ile Val
355 360 365

Gly Asn Val Gly Ser Met Ile Ser Asn Met Asn Ala Thr Arg Ala Glu
370 375 380

Phe Gln Ala Lys Ile Asp Ala Val Lys His Tyr Met Gln Phe Arg Lys
385 390 395 400

Val Ser Lys Gly Met Glu Ala Lys Val Ile Arg Trp Phe Asp Tyr Leu
405 410 415

Trp Thr Asn Lys Lys Thr Val Asp Glu Arg Glu Ile Leu Lys Asn Leu
420 425 430

Pro Ala Lys Leu Arg Ala Glu Ile Ala Ile Asn Val His Leu Ser Thr
435 440 445

Leu Lys Lys Val Arg Ile Phe His Asp Cys Glu Ala Gly Leu Leu Val
450 455 460

Glu Leu Val Leu Lys Leu Arg Pro Gln Val Phe Ser Pro Gly Asp Tyr
465 470 475 480

Ile Cys Arg Lys Gly Asp Ile Gly Lys Glu Met Tyr Ile Ile Lys Glu
485 490 495

Gly Lys Leu Ala Val Val Ala Asp Asp Gly Val Thr Gln Tyr Ala Leu
500 505 510

Leu Ser Ala Gly Ser Cys Phe Gly Glu Ile Ser Ile Leu Asn Ile Lys
515 520 525

Gly Ser Lys Met Gly Asn Arg Arg Thr Ala Asn Ile Arg Ser Leu Gly
530 535 540

Tyr Ser Asp Leu Phe Cys Leu Ser Lys Asp Asp Leu Met Glu Ala Val
545 550 555 560

Thr Glu Tyr Pro Asp Ala Lys Lys Val Leu Glu Glu Arg Gly Arg Glu
565 570 575

Ile Leu Met Lys Glu Gly Leu Leu Asp Glu Asn Glu Val Ala Thr Ser
580 585 590

Met Glu Val Asp Val Gln Glu Lys Leu Gly Gln Leu Glu Thr Asn Met
595 600 605

Glu Thr Leu Tyr Thr Arg Phe Gly Arg Leu Leu Ala Glu Tyr Thr Gly
610 615 620

Ala Gln Gln Lys Leu Lys Gln Arg Ile Thr Val Leu Glu Thr Lys Met
625 630 635 640

Lys Gln Asn Asn Glu Asp Asp Tyr Leu Ser Asp Gly Met Asn Ser Pro

645

650

655

Glu Leu Ala Ala Ala Asp Glu Pro
660